

INPUT SET: S34734.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING
23 (1) General Information: ENTERED4
5 (i) APPLICANT: Borts, Tracy L.
6 Broderick, Carol L.
7 DiMarchi, Richard D.
8 Grinnell, Brian W.
9 Miller, Anne R.10
11 (ii) TITLE OF INVENTION: DIABETES THERAPY12
13 (iii) NUMBER OF SEQUENCES: 914
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Eli Lilly and Company
17 (B) STREET: Lilly Corporate Center
18 (C) CITY: Indianapolis
19 (D) STATE: Indiana
20 (E) COUNTRY: USA
21 (F) ZIP: 4628522
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.3028
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:US/09/091,605
31 (B) FILING DATE: 16-JUN-1998
32 (C) CLASSIFICATION:514
3334
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Davis, Steven G.
37 (B) REGISTRATION NUMBER: 39,652
38 (C) REFERENCE/DOCKET NUMBER: X-987239
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: (617) 250-1833
42 (B) TELEFAX: (617) 354-635543
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47 (A) LENGTH: 31 amino acids
48 (B) TYPE: amino acid
49 (C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear
51
52 (ii) MOLECULE TYPE: protein
53
54
55 (ix) FEATURE:
56 (A) NAME/KEY: Modified-site
57 (B) LOCATION: 2
58 (D) OTHER INFORMATION: /note= "Xaa at position 2 is Ala,
59 Gly, Val, Thr, and Ile"
60
61 (ix) FEATURE:
62 (A) NAME/KEY: Modified-site
63 (B) LOCATION: 15
64 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Glu,
65 Gln, Ala, Thr, Ser, and Gly"
66
67 (ix) FEATURE:
68 (A) NAME/KEY: Modified-site
69 (B) LOCATION: 20
70 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Lys,
71 and Arg"
72
73 (ix) FEATURE:
74 (A) NAME/KEY: Modified-site
75 (B) LOCATION: 21
76 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Glu,
77 Gln, Ala, Thr, Ser, and Gly; and,"
78
79 (ix) FEATURE:
80 (A) NAME/KEY: Modified-site
81 (B) LOCATION: 31
82 (D) OTHER INFORMATION: /note= "Xaa at position 31 is
83 Gly-OH or is absent"
84
85
86 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
87
88 His Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly
89 1 5 10 15
90
91 Gln Ala Ala Xaa Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
92 20 25 30
93
94 (2) INFORMATION FOR SEQ ID NO:2:
95
96 (i) SEQUENCE CHARACTERISTICS:
97 (A) LENGTH: 93 base pairs
98 (B) TYPE: nucleic acid
99 (C) STRANDEDNESS: single

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100 (D) TOPOLOGY: linear
101
102 (ii) MOLECULE TYPE: cDNA
103
104
105 (ix) FEATURE:
106 (A) NAME/KEY: CDS
107 (B) LOCATION: 1..93
108
109
110 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
111
112 CAT GCT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG GAA GGC 48
113 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
114 1 5 10 15
115
116 CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA GGC CGA GGA 93
117 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
118 20 25 30
119
120
121 (2) INFORMATION FOR SEQ ID NO:3:
122
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 31 amino acids
125 (B) TYPE: amino acid
126 (D) TOPOLOGY: linear
127
128 (ii) MOLECULE TYPE: protein
129
130 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
131
132 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
133 1 5 10 15
134
135 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
136 20 25 30
137
138 (2) INFORMATION FOR SEQ ID NO:4:
139
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 93 base pairs
142 (B) TYPE: nucleic acid
143 (C) STRANDEDNESS: single
144 (D) TOPOLOGY: linear
145
146 (ii) MOLECULE TYPE: cDNA
147
148
149 (ix) FEATURE:
150 (A) NAME/KEY: CDS
151 (B) LOCATION: 1..93
152

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153
154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
155
156 CAT GTT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG GAA GGC 48
157 His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
158 1 5 10 15
159
160 CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA GGC CGA GGA 93
161 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
162 20 25 30
163
164 (2) INFORMATION FOR SEQ ID NO:5:
165
166 (i) SEQUENCE CHARACTERISTICS:
167 (A) LENGTH: 31 amino acids
168 (B) TYPE: amino acid
169 (D) TOPOLOGY: linear
170
171 (ii) MOLECULE TYPE: protein
172
173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
174
175 His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
176 1 5 10 15
177
178 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
179 20 25 30
180
181 (2) INFORMATION FOR SEQ ID NO:6:
182
183 (i) SEQUENCE CHARACTERISTICS:
184 (A) LENGTH: 105 base pairs
185 (B) TYPE: nucleic acid
186 (C) STRANDEDNESS: single
187 (D) TOPOLOGY: linear
188
189 (ii) MOLECULE TYPE: cDNA
190
191
192
193
194 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
195
196 GACATGCTGA AGGGACCTTT ACCAGTGATG TAAGTTCTTA TTTGGAAGGC CAAGCTGCCA 60
197
198 AGGAATTCA TGCTTGGCTG GTGAAAGGCC GAGGATAGGG ATCCC 105
199
200
201 (2) INFORMATION FOR SEQ ID NO:7:
202
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 109 base pairs
205 (B) TYPE: nucleic acid

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206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear

208
209 (ii) MOLECULE TYPE: cDNA
210
211
212
213
214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
215
216 CTAGGGGATC CCTATCCTCG GCCTTCACC AGCCAAGCAA TGAATTCTT GGCAGCTTGG 60
217
218 CCTTCCAAAT AAGAACTTAC ATCACTGGTA AAGGTCCCTT CAGCATGTC 109
219
220 (2) INFORMATION FOR SEQ ID NO:8:
221
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 105 base pairs
224 (B) TYPE: nucleic acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
227
228 (ii) MOLECULE TYPE: cDNA
229
230
231
232
233 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
234
235 GACATGTTGA AGGGACCTTT ACCAGTGATG TAAGTTCTTA TTTGGAAGGC CAAGCTGCCA 60
236
237 AGGAATTCAAT TGCTTGGCTG GTGAAAGGCC GAGGATAGGG ATCCC 105
238
239 (2) INFORMATION FOR SEQ ID NO:9:
240
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 109 base pairs
243 (B) TYPE: nucleic acid
244 (C) STRANDEDNESS: single
245 (D) TOPOLOGY: linear
246
247 (ii) MOLECULE TYPE: DNA (genomic)
248
249
250
251
252 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
253
254 CTAGGGGATC CCTATCCTCG GCCTTCACC AGCCAAGCAA TGAATTCTT GGCAGCTTGG 60
255
256 CCTTCCAAAT AAGAACTTAC ATCACTGGTA AAGGTCCCTT CAACATGTC 109
257
258

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SEQUENCE VERIFICATION REPORT
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Line	Error	Original Text
32	Wrong Classification	(C) CLASSIFICATION:514